

	Query Match	100.0%;	Score 1120;	DB 2;	Length 1120;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 1120;	Conservative	0;	Mismatches	0; Indels
					0; Gaps
QY	1	CACAGGGTGAAGCTTTGGTTCTCTGCTGCTGTAAACAGGGACTTAGCACACACACGGAT	60		
DB	1	CACAGGGTGAAGCTTTGGTTCTCTGCTGCTGTAAACAGGGACTTAGCACACACACGGAT	60		
QY	61	GAGTGGGGTCATTTCACAGATATTAGGTCAACAGCAGAGAAGCAGCCAAAATGGATCCCCAGTG	120		
DB	61	GAGTGGGGTCATTTCACAGATATTAGGTCAACAGCAGAGAAGCAGCCAAAATGGATCCCCAGTG	120		
QY	121	CACATATGGGACTGAGTAAACATTCCTCTTTTGATGGGCTTCCTGCTCTCTGGTGGCTGCTCC	180		
DB	121	CACATATGGGACTGAGTAAACATTCCTCTTTTGATGGGCTTCCTGCTCTCTGGTGGCTGCTCC	180		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 12:25:16 ; Search time 87.5067 Seconds
(without alignments)
7102.827 Million cell updates/sec

Title: US-09-962-969B-22
Perfect score: 1120
Sequence: 1 CACAGGTCGAAGCTTCTCT.....AGAGTAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1120	100.0	1120	2	US-08-456-104-1
2	1120	100.0	1120	2	US-08-101-624-1
3	1120	100.0	1120	3	US-08-479-744A-1
4	1120	100.0	1120	3	US-08-280-757B-1
5	1120	100.0	1120	3	US-08-305-697A-22
6	1120	100.0	1120	3	US-08-702-525-22
7	1120	100.0	1120	4	US-08-403-253A-3
8	1120	100.0	1120	4	US-08-435-816A-3
9	1120	100.0	1120	4	US-09-425-762-1
10	1120	100.0	1120	4	US-09-837-867A-22
11	1120	100.0	1120	5	PCT-US95-02576-22
12	1014.8	90.6	1161	3	US-08-205-697A-24
13	1014.8	90.6	1161	3	US-08-702-525-24
14	1014.8	90.6	1161	4	US-09-837-867A-24
15	1014.8	90.6	1161	5	PCT-US95-02576-24
16	995.8	88.9	1424	4	US-09-326-186B-226
17	995.8	88.9	1428	5	PCT-US94-09642-1
18	990	88.4	1002	3	US-09-039-982A-33
19	990	88.4	1002	3	US-09-039-641-33
20	990	88.4	1002	3	US-09-039-762A-33
21	990	88.4	1002	4	US-09-042-492D-33
22	990	88.4	1002	4	US-08-913-612A-33
23	972	86.8	972	3	US-08-848-760B-11
24	738	65.9	751	3	US-09-039-982A-34
25	738	65.9	751	3	US-09-039-641-34
26	738	65.9	751	3	US-09-039-762A-34
27	738	65.9	751	4	US-09-042-492D-34

28 738 65.9 751 4 US-08-913-612A-34
29 533.2 47.6 1080 4 US-09-103-040-5
30 407.2 36.4 1151 2 US-08-456-104-3
31 407.2 36.4 1151 3 US-08-205-697A-20
32 407.2 36.4 1151 3 US-08-702-525-20
33 407.2 36.4 1151 4 US-09-837-867A-20
34 407.2 36.4 1151 5 PCT-US95-02576-20
35 407.2 36.4 1163 3 US-08-479-744A-22
36 407.2 36.4 1163 3 US-08-280-757B-22
37 407.2 36.4 1183 4 US-09-425-762-22
38 394 35.2 1251 3 US-08-305-697A-12
39 394 35.2 1261 3 US-08-702-525-12
40 394 35.2 1261 4 US-09-837-867A-12
41 394 35.2 1261 5 PCT-US95-02576-12
42 325.2 29.0 330 3 US-08-479-744A-44
43 325.2 29.0 330 3 US-08-280-757B-44
44 325.2 29.0 330 4 US-09-425-762-44
45 306 27.3 306 3 US-08-479-744A-46

ALIGNMENTS

RESULT 1
US-08-456-104-1
; Sequence 1, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 424
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1120 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..1093
US-08-456-104-1

Sequence 34, Appl
Sequence 5, Appl
Sequence 3, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 46, Appl

APPLICATION NUMBER: US 07/864,805
 FILING DATE: 7-APR-1992
 APPLICATION NUMBER: US 08/247,505
 FILING DATE: 23-MAY-1994
 APPLICATION NUMBER: US 07/864,866
 FILING DATE: 7-APR-1992
 APPLICATION NUMBER: US 08/218,155
 FILING DATE: 25-MAR-1994
 APPLICATION NUMBER: US 07/864,807
 FILING DATE: 7-APR-1992
 APPLICATION NUMBER: US 07/902,467
 FILING DATE: 16-JUNE-1992
 APPLICATION NUMBER: US 07/275,433
 FILING DATE: 23-NOV-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-002CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1120 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 107..1093
 US-08-592-711-3

Query Match 100.0%; Score 1120; DB 8; Length 1120;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGGGTGAAGAGCTTTGGTCTCTGCTGTGTAAACAGGAGCTAGCAGACACACGGAT 60
 DB 1 CACAGGGTGAAGAGCTTTGGTCTCTGCTGTGTAAACAGGAGCTAGCAGACACACGGAT 60

QY 61 GAGTGGGTGCTATTCAGATATAGTGTACAGACAGAGCCAAATGGATCCCGAGTG 120
 DB 61 GAGTGGGTGCTATTCAGATATAGTGTACAGACAGAGCCAAATGGATCCCGAGTG 120

QY 121 CACTATGGAGCTGAGTAAACATCTCTTGTGATGCGCTCTCTGCTCTCTGCTGCTGCC 180
 DB 121 CACTATGGAGCTGAGTAAACATCTCTTGTGATGCGCTCTCTGCTCTCTGCTGCTGCC 180

QY 181 TCTGAAGATCAAGCTTATTTCAATGAGACTGCGACCTGCGATGCCCAATTTGCAAACTC 240
 DB 181 TCTGAAGATCAAGCTTATTTCAATGAGACTGCGACCTGCGATGCCCAATTTGCAAACTC 240

QY 241 TCAAAACCAAGCCCTGAGTGAGCTAGTACTATTTTGGCAGGACCAAGGAAACTTGGTTCT 300
 DB 241 TCAAAACCAAGCCCTGAGTGAGCTAGTACTATTTTGGCAGGACCAAGGAAACTTGGTTCT 300

QY 301 GAATGAGGTATCTAGGCAAGAGAAATTTGACAGTGTTCATTTCCAAAGTATATGGCGCG 360
 DB 301 GAATGAGGTATCTAGGCAAGAGAAATTTGACAGTGTTCATTTCCAAAGTATATGGCGCG 360

QY 361 CACAGTTTTGATTCGGACAGTTGGACCTGAGCTTCCACATCTTCAGATCAAGGACAA 420
 DB 361 CACAGTTTTGATTCGGACAGTTGGACCTGAGCTTCCACATCTTCAGATCAAGGACAA 420

QY 421 GGGCTTGATCAATGATATCATCCATCACAAAAGCCACAGGAATGATTCGCATCCACCA 480
 DB 421 GGGCTTGATCAATGATATCATCCATCACAAAAGCCACAGGAATGATTCGCATCCACCA 480

QY 481 GATGAATTCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 DB 481 GATGAATTCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 541 TAATATAACAGAAAATGTGTACATAAATTTGACCTGCTCATCTATACACGGTTACCCAGA 600
 DB 541 TAATATAACAGAAAATGTGTACATAAATTTGACCTGCTCATCTATACACGGTTACCCAGA 600

QY 601 ACCTAAGAAGATGAGTGTGTTTGTCTAAGAACCAGAAATTCAACTATCGAGTATGATGGTAT 660
 DB 601 ACCTAAGAAGATGAGTGTGTTTGTCTAAGAACCAGAAATTCAACTATCGAGTATGATGGTAT 660

QY 661 TATGCAGAAAATCTCAAGATAATGTACAGAACTGTACGACGTTTCCATCAGCTTGTCTGT 720
 DB 661 TATGCAGAAAATCTCAAGATAATGTACAGAACTGTACGACGTTTCCATCAGCTTGTCTGT 720

QY 721 TTCAATCCCTGATGTTACGAGCAATATGACCATCTCTCTGTTATTTCTGAAAACCTGACAAGAC 780
 DB 721 TTCAATCCCTGATGTTACGAGCAATATGACCATCTCTCTGTTATTTCTGAAAACCTGACAAGAC 780

QY 781 GCGGCTTTTATCTTCACCTTTCTCTATAGAGCTTGGAGCCCTCAGCTTCCCGCCAGACCA 840
 DB 781 GCGGCTTTTATCTTCACCTTTCTCTATAGAGCTTGGAGCCCTCAGCTTCCCGCCAGACCA 840

QY 841 CATTCCTTGGATTACAGCTGTACTTCCAAACAGTATTTATATGTTGATGTTGTTTCTGTCT 900
 DB 841 CATTCCTTGGATTACAGCTGTACTTCCAAACAGTATTTATATGTTGATGTTGTTTCTGTCT 900

QY 901 AATTCTATGGAATGGAAGAAGAGCGGCTCGCAACTCTTTATAATGTGGAACCAA 960
 DB 901 AATTCTATGGAATGGAAGAAGAGCGGCTCGCAACTCTTTATAATGTGGAACCAA 960

QY 961 CACAATGGAGAGGAGAGAGTGAACAGACCAAGAAAGAAAATCCATATACCTGA 1020
 DB 961 CACAATGGAGAGGAGAGAGTGAACAGACCAAGAAAGAAAATCCATATACCTGA 1020

QY 1021 AAGATCTGATGAAGCCAGCGTGTGTTTAAAGTTCGAAAGACATCTTCATGCGACAAAAG 1080
 DB 1021 AAGATCTGATGAAGCCAGCGTGTGTTTAAAGTTCGAAAGACATCTTCATGCGACAAAAG 1080

QY 1081 TGATACATGTTTTTAATTAAGAGTAAAGCCCAAAAAA 1120
 DB 1081 TGATACATGTTTTTAATTAAGAGTAAAGCCCAAAAAA 1120

RESULT 2

US-09-837-867A-22
 ; Sequence 22, Application US/09837867A
 ; Patent No. US20020098542A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sharpe, Arlene H.
 ; APPLICANT: Borriello, Francescopaulo
 ; APPLICANT: Freeman, Gordon J.
 ; APPLICANT: Nadler, Lee M.
 ; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
 ; FILE REFERENCE: BWI-120CPADV
 ; CURRENT APPLICATION NUMBER: US/09/837,867A
 ; CURRENT FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 08/205,697
 ; PRIOR FILING DATE: 1994-03-02
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 1120
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (107) ... (1093)
 ; US-09-837-867A-22

Query Match 100.0%; Score 1120; DB 9; Length 1120;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACAGGGTGAAGAGCTTTGGTCTCTGCTGTGTAAACAGGAGCTAGCAGACACACGGAT 60

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1120	100.0	1120	2	AAQ81351	1	AaQ81351 Human B 1
2	1120	100.0	1120	2	AA49181	1	Aa49181 Human B 1
3	1120	100.0	1120	2	AAV55784	1	AaV55784 Human B7-
4	1120	100.0	1120	3	AA684049	1	Aa684049 Human B 1
5	1120	100.0	1120	6	ABV72340	1	AbV72340 Nucleotid
6	1120	100.0	1120	6	AAQ27968	1	AaQ27968 Human B7-
7	1120	100.0	1120	9	AAD60374	1	AaD60374 Human CD2
8	995.8	88.9	1424	3	AA229321	1	Aa229321 Human B7.
9	995.8	88.9	1424	6	ABU64578	1	AbU64578 Stomach c
10	995.8	88.9	1424	6	ABU63096	1	AbU63096 Breast ca
11	995.8	88.9	1424	6	ABX84193	1	AbX84193 Human cDN
12	995.8	88.9	1424	9	AD225559	1	Ad225559 Binding d
13	995.8	88.9	1428	2	AAQ85873	1	AaQ85873 B70 type
14	995.8	88.9	2205	4	AAH72616	1	AaH72616 Human cer
15	972	86.8	972	2	AAV83208	1	AaV83208 B7-2 cDNA
16	972	86.8	972	6	AAQ25510	1	AaQ25510 Human co-
17	753.2	67.2	831	2	AAV03230	1	AaV03230 DNA encod
18	723.4	64.6	738	2	AAV80293	1	AaV80293 Human B7-
19	723.4	64.6	738	4	AAE89731	1	AaE89731 Nucleotid
20	597	53.3	1897	2	AA227914	1	Aa227914 Canine B7
21	597	53.3	1897	2	AA227913	1	Aa227913 Canine B7
22	575.2	51.4	987	2	AA227915	1	Aa227915 Canine B7
23	575.2	51.4	987	2	AA227916	1	Aa227916 Complemen

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OM nucleic - nucleic search, using sw model
Run on: March 20, 2004, 11:47:41 ; Search time 3206.43 Seconds
(without alignments)
10430.790 Million cell updates/sec

Title: US-09-962-969B-22
Perfect score: 1120
Sequence: 1 CACAGGCTAAAGCTTTGCT.....ACAGTAAAGCCCAAAAAA 1120

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
- 4: em_estnu.*
- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hct.*
- 9: gb_est1.*
- 10: gb_est2.*
- 11: gb_hct.*
- 12: gb_est3.*
- 13: gb_est4.*
- 14: gb_est5.*
- 15: em_estfun.*
- 16: em_estom.*
- 17: em_gss_hum.*
- 18: em_gss_inv.*
- 19: em_gss_pln.*
- 20: em_gss_vrt.*
- 21: em_gss_fun.*
- 22: em_gss_man.*
- 23: em_gss_mus.*
- 24: em_gss_pro.*
- 25: em_gss_rod.*
- 26: em_gss_phg.*
- 27: em_gss_vrl.*
- 28: gb_gss1.*
- 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	683	61.0	709	13 BQ109553	BQ109553 imageqc 7
2	679.8	60.7	753	12 B1306246	B1306246 603063172
3	645	57.7	889	13 BX396966	BX396966 BX396966
4	598.6	53.4	655	12 B1824940	B1824940 603032554

C	5	588.8	52.6	926	13	BX371662	BX371662
	6	470.4	42.0	680	14	CD688144	EST4566 h
	7	448.4	40.0	490	14	CD698408	EST14931
C	8	426.6	38.1	925	13	BX351622	BX351622
	9	407.2	36.4	2541	11	AK079513	Mus muscu
	10	400.8	35.8	496	10	AW516826	AW516826 XQ401.x
	11	377	33.7	595	14	CD705810	EST22337
	12	350.4	31.3	658	14	CB288199	CB288199 CMD76_C10
	13	325.4	29.1	347	10	BG001664	BG001664 RC4-GN006
	14	323.6	28.9	675	13	BY749883	BY749883
	15	316.4	28.2	629	10	B8631711	B8631711
	16	311.4	27.8	1002	10	BF137460	BF137460 601780644
	17	299.6	26.8	448	9	AA056906	AA056906 EST224R P
C	18	276.4	24.7	565	12	BQ002799	BQ002799 UI-H-B11-
	19	268.2	23.9	543	10	BF064222	BF064222 757b02.x
	20	259.8	23.2	578	12	BM089797	BM089797 503647 MA
C	21	258.4	23.1	570	9	AI093604	AI093604 ou82b09.s
	22	250	22.3	576	14	CD471494	CD471494 Leuko55_6
	23	245.2	21.9	736	29	CE294610	CE294610 tigr-g88
	24	243.6	21.8	580	14	CB472621	CB472621 sn57_G10.
C	25	233.8	20.9	580	14	CB472663	CB472663 sn58_D09.
	26	227.6	20.3	654	10	B8635605	B8635605
	27	224.2	20.0	504	9	AA946810	AA946810 og43c01.s
C	28	222.2	19.8	418	14	CD468511	CD468511 Leuko53_3
	29	211.2	18.9	345	29	CG542494	CG542494 OST137097
	30	205	18.3	220	14	CD523014	CD523014 AGENCOURT
	31	192.4	17.2	380	14	CB810508	CB810508 AMGNOC:M
C	32	178	15.9	512	9	AA056905	AA056905 EST224F P
	33	175.6	15.7	374	13	BY221563	BY221563
	34	174.8	15.6	377	13	BY179845	BY179845
C	35	172.2	15.4	480	9	AI750143	AI750143 at27h10.x
	36	172	15.4	690	13	BQ109523	BQ109523 imageqc 7
	37	172	15.4	695	12	BI767024	BI767024 603054234
	38	167.8	15.0	362	13	BY203663	BY203663
	39	164	14.6	705	13	BY764599	BY764599
	40	163.8	14.6	366	13	BY221252	BY221252
	41	163.2	14.6	257	10	AW479222	AW479222 64549 MAR
	42	160.6	14.3	351	13	BY163388	BY163388
	43	156.2	13.9	344	13	BY175601	BY175601
	44	155.2	13.9	357	13	BY187789	BY187789
	45	154.8	13.8	353	13	BY193840	BY193840

ALIGNMENTS

RESULT 1
BQ109553
LOCUS
DEFINITION imageqc 7 2001/snm58bdr81.y1 NIH_MGC_118 Homo sapiens cDNA clone
ACCESSION BQ109553
VERSION BQ109553.1 GI:20159207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 709)
AUTHORS Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and Prange,C.K.
TITLE The I.M.A.G.E. Consortium quality control effort: clone
JOURNAL resequencing for verification
COMMENT Unpublished (2001)
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been produced as part of the I.M.A.G.E. Consortium
quality control effort. High quality sequence is defined as having
100 or more base pairs with a phred quality value of 20 or greater,
where a sliding window of 4 base pairs with a phred quality value

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 12:21:06 ; Search time 4548.2 Seconds
(without alignments)
10673.268 Million cell updates/sec

Title: US-09-962-969b-22
Perfect score: 1120
Sequence: 1 CACAGGGTGAAGCTTGTCT.....AGAGTAAAGCCCAAAAAA 1120

Scoring table: IDENTITY_NUC
Gapop 10_0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_hg_hum.*

31: em_hg_inv.*

32: em_hg_other.*

33: em_hg_mus.*

34: em_hg_pln.*

35: em_hg_rtd.*

36: em_hg_mam.*

37: em_hg_vrt.*

38: em_sy.*

39: em_hgo_hum.*

40: em_hgo_mus.*

41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1120	100.0	1120	6	AR030780	AR030780 Sequence
2	1120	100.0	1120	6	AR112747	AR112747 Sequence
3	1120	100.0	1120	6	AR146413	AR146413 Sequence
4	1120	100.0	1120	6	BD272169	BD272169 Use of so
5	1120	100.0	1120	6	AR196804	AR196804 Sequence
6	1120	100.0	1120	6	AR287728	AR287728 Sequence
7	1120	100.0	1120	6	AR374141	AR374141 Sequence
8	1120	100.0	1120	6	AR381495	AR381495 Sequence
9	1120	100.0	1120	6	AX047043	AX047043 Sequence
10	1113.2	99.4	2781	9	BC040261	BC040261 Homo sapi
11	1112	99.3	1112	9	HUMB72A	L25259 Human CTLA4
12	1014.8	90.6	1161	6	AR146414	AR146414 Sequence
13	1014.8	90.6	1161	6	AR381496	AR381496 Sequence
14	995.8	88.9	1424	6	AR178980	AR178980 Sequence
15	995.8	88.9	1424	6	BD267799	BD267799 Methods a
16	995.8	88.9	1424	6	AX330924	AX330924 Sequence
17	995.8	88.9	1424	6	AX332506	AX332506 Sequence
18	995.8	88.9	1424	9	HSU04343	U04343 Human CD86
19	995.8	88.9	2205	6	AX188198	AX188198 Sequence
20	990	88.4	1002	6	AR147736	AR147736 Sequence
21	990	88.4	1002	6	AR159758	AR159758 Sequence
22	990	88.4	1002	6	AR160450	AR160450 Sequence
23	990	88.4	1002	6	AR202406	AR202406 Sequence
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25	972	86.8	972	6	BD237348	BD237348 Improve
26	972	86.8	972	6	AX027005	AX027005 Sequence
27	972	86.8	972	6	BD105961	BD105961 Animal mo
28	944	84.3	1048	9	AF344857	AF344857 Macaca mu
29	936.6	83.6	1062	9	AF344861	AF344861 Cercopith
30	933.4	83.3	1062	9	AF344840	AF344840 Cercocebu
31	931.8	83.2	1044	9	AF344851	AF344851 Macaca ne
32	738	65.9	751	6	AR147737	AR147737 Sequence
33	738	65.9	751	6	AR159759	AR159759 Sequence
34	738	65.9	751	6	AR160451	AR160451 Sequence
35	738	65.9	751	6	AR202407	AR202407 Sequence
36	738	65.9	751	6	AR235984	AR235984 Sequence
37	723.4	64.6	738	6	AX002781	AX002781 Sequence
38	723.4	64.6	738	6	AX149548	AX149548 Sequence
39	723.4	64.6	738	6	BD136153	BD136153 Vector. 9
40	652.6	58.3	901	9	AF344836	AF344836 Papio cyn
41	597	53.3	1897	4	AF106826	AF106826 Canis fam
42	567.2	50.6	1156	4	RABCD86B	D49842 Oryctolagus
43	560.2	50.0	1270	4	AB030652	AB030652 Felis cat
44	558.6	49.9	2830	4	AY007704	AY007704 Felis cat
45	537	47.9	994	4	PIGCD86G	L76099 Sus scrofa

ALIGNMENTS

RESULT 1	AR030780	1120 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 1 from patent US 5861310.				
DEFINITION	Sequence 1 from patent US 5861310.				
ACCESSION	AR030780				
VERSION	AR030780.1	GI:5943994			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				

REFERENCE 1 (bases 1 to 1120)
Freeman,G.J., Nadler,L.M. and Gray,G.S.
Tumor cells modified to express B7-2 with increased immunogenicity
and uses therefor
Patent: US 5861310-A 1 19-JAN-1999;
JOURNAL

CELL TYPE: B cell
CELL LINE: Raji
IMMEDIATE SOURCE:
LIBRARY: cDNA in pCDMS vector
CLONE: B7, Raji clone #13
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
NAME/KEY: Open reading frame (translated region)
LOCATION: 318 to 1181 bp
IDENTIFICATION METHOD: similarity to other pattern
FEATURE:
NAME/KEY: Alternate polyadenylation signal
LOCATION: 1474 to 1479 bp
IDENTIFICATION METHOD: similarity to other pattern
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplast
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491
US-08-147-772-1

[illegible]

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US-08-45
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; Patent
; GENER
; APP
; APP
; APP
; TIT

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661	QY	AGTGTTGTTCTCGAAGTATGAAGAAGAGCGTTTCAAGCGGAAACACCTGGCTGAAGTGA	720
661	DB	AGTGTTGTTCTCGAAGTATGAAGAAGAGCGTTTCAAGCGGAAACACCTGGCTGAAGTGA	720
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901	QY	CTGAGCTCTATGCTGTAGCAGCAACTGGATTCAATATGACAAACCAACACAGCTTCA	960
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961	QY	TGTGTCCTCAAGTATGACATTTAAAGTAGTAATCAGACCTTCAACTGGAATACAACCA	1020
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1021	QY	AGCAAGACATTTTCTGTATACCTGCTCCCATCTCGGGCCATTACCTTAATCTCAGTAA	1080
1021	DB	AGCAAGACATTTTCTGTATACCTGCTCCCATCTCGGGCCATTACCTTAATCTCAGTAA	1080
1081	QY	ATGGAATTTTGTGATATGCTGCTGACCTACTGCTTTTCCCAAGATCGAGAGAGAA	1140
1081	DB	ATGGAATTTTGTGATATGCTGCTGACCTACTGCTTTTCCCAAGATCGAGAGAGAA	1140
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1141	DB	GAGGAAATGAGAGATTGAGAAAGGAAGTGAAGCCCTGTATAACAGTGTCCCGAGAGC	1200
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1201	DB	AAGGGGCTGAAAGAATCTGAAGGTAGCCTCCGTCATCTCTCTGGGATACATGATCGTG	1260
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1321	QY	CTTAAAAACCTCTTTTCAGATTAAGCTGAACAGTTCACAAGATGGCTGGCATCCCTCTCCTT	1380
1321	DB	CTTAAAAACCTCTTTTCAGATTAAGCTGAACAGTTCACAAGATGGCTGGCATCCCTCTCCTT	1380
1381	QY	TCTCCCATATGCAATTTGCTTAATGTAACCTCTCTTTGGCATGTTTCCATCTTCGCCA	1440
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1441	QY	TCTTGAATTTGCTGTGTCAGCAATTCATTATCTATTAAACACTAAATTTGAG	1491
1441	DB	TCTTGAATTTGCTGTGTCAGCAATTCATTATCTATTAAACACTAAATTTGAG	1491

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 12:25:16 ; Search time 116.493 Seconds
(without alignments)
7102.827 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1491	100.0	1491	2	US-08-456-104-5 Sequence 5, Appl
3	1491	100.0	1491	2	US-08-101-624-22 Sequence 22, Appl
4	1491	100.0	1491	3	US-08-153-262-1 Sequence 1, Appl
5	1491	100.0	1491	3	US-08-479-744A-28 Sequence 28, Appl
6	1491	100.0	1491	3	US-08-280-757B-28 Sequence 28, Appl
7	1491	100.0	1491	3	US-09-159-135-1 Sequence 1, Appl
8	1491	100.0	1491	3	US-08-205-697A-18 Sequence 18, Appl
9	1491	100.0	1491	3	US-08-702-525-18 Sequence 18, Appl
10	1491	100.0	1491	4	US-09-450-798-1 Sequence 1, Appl
11	1491	100.0	1491	4	US-08-403-253A-1 Sequence 1, Appl
12	1491	100.0	1491	4	US-08-435-816A-1 Sequence 1, Appl
13	1491	100.0	1491	4	US-09-425-762-28 Sequence 28, Appl
14	1491	100.0	1491	4	US-09-837-867A-18 Sequence 18, Appl
15	1491	100.0	1491	4	US-08-453-386A-1 Sequence 1, Appl
16	1491	100.0	1491	5	PCT-US95-02576-18 Sequence 18, Appl
17	1489.4	99.9	1491	2	US-08-751-767A-5 Sequence 5, Appl
18	1489.4	99.9	1491	4	US-09-326-186B-225 Sequence 225, App
19	868.2	58.2	879	3	US-09-039-982A-31 Sequence 31, Appl
20	868.2	58.2	879	3	US-09-039-641-31 Sequence 31, Appl
21	868.2	58.2	879	3	US-09-039-762A-31 Sequence 31, Appl
22	868.2	58.2	879	4	US-09-042-492D-31 Sequence 31, Appl
23	868.2	58.2	879	4	US-08-913-612A-31 Sequence 31, Appl
24	865.4	58.0	867	2	US-08-184-009-207 Sequence 207, App
25	865.4	58.0	867	2	US-08-458-356-207 Sequence 207, App
26	865.4	58.0	867	3	US-08-460-736-207 Sequence 207, App
27	865.4	58.0	867	4	US-09-495-052-59 Sequence 59, Appl

28	865.4	58.0	867	4	US-09-535-370-207 Sequence 207, App
29	863.8	57.9	867	3	US-08-812-948A-2 Sequence 2, Appl
30	820.6	55.0	867	4	US-09-495-052-60 Sequence 60, Appl
31	727.2	48.8	738	3	US-09-039-982A-32 Sequence 32, Appl
32	727.2	48.8	738	3	US-09-039-641-32 Sequence 32, Appl
33	727.2	48.8	738	3	US-09-039-762A-32 Sequence 32, Appl
34	727.2	48.8	738	4	US-09-042-492D-32 Sequence 32, Appl
35	727.2	48.8	738	4	US-08-913-612A-32 Sequence 32, Appl
36	726.6	48.7	1446	3	US-09-171-945-130 Sequence 130, App
37	721.2	48.4	1428	3	US-08-812-948A-3 Sequence 3, Appl
38	465.2	31.2	941	4	US-09-303-040-1 Sequence 1, Appl
39	452.8	30.4	879	4	US-09-303-040-3 Sequence 3, Appl
40	416.4	27.9	900	4	US-09-495-052-61 Sequence 61, Appl
41	416	27.9	416	3	US-08-205-697A-35 Sequence 35, Appl
42	416	27.9	416	3	US-08-702-525-35 Sequence 35, Appl
43	416	27.9	416	4	US-09-837-867A-35 Sequence 35, Appl
44	416	27.9	416	5	PCT-US95-02576-35 Sequence 35, Appl
45	379	25.4	379	3	US-08-205-697A-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-147-772-1
; Sequence 1, Application US/08147772
; Patent No. 5858776
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: lymphoid

APPLICATION NUMBER: US 07/864,805	Qy	61	GGAGTCTTACCTCGAAATCAAGGATTTAAAGAAAAGTGGAAATTTTCTTTCAGCAAGCT	120
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APPLICATION NUMBER: US 08/247,505	Qy	121	GTGAAACTAAATCCCAACCTTTTGAGACCCAGGAAACACCTCCCAATCTCTGTGTGTTTT	180
FILING DATE: 23-MAY-1994	Db	121	GTGAAACTAAATCCCAACCTTTTGAGACCCAGGAAACACCTCCCAATCTCTGTGTGTTTT	180
APPLICATION NUMBER: US 07/864,866	Qy	181	GTAACATCACTGGAGGGTCTTCTAGTGAGCAATGGATTTGATCATCAGCCCTGCTGTT	240
FILING DATE: 7-APR-1992	Db	181	GTAACATCACTGGAGGGTCTTCTAGTGAGCAATGGATTTGATCATCAGCCCTGCTGTT	240
APPLICATION NUMBER: US 08/218,155	Qy	241	TTGCACCTGGGAAGTCCCTGCTCTTACCTTGGGTCCAAATTTGCTTTCACCTTTTGAC	300
FILING DATE: 25-MAR-1994	Db	241	TTGCACCTGGGAAGTCCCTGCTCTTACCTTGGGTCCAAATTTGCTTTCACCTTTTGAC	300
APPLICATION NUMBER: US 07/864,907	Qy	301	CCTAAGCATCTGAAGCCATGGGCCACACAGGAGGAGGGAACATCACCATCAAGTGTG	360
FILING DATE: 7-APR-1992	Db	301	CCTAAGCATCTGAAGCCATGGGCCACACAGGAGGAGGGAACATCACCATCAAGTGTG	360
APPLICATION NUMBER: US 07/902,467	Qy	361	CATACCTGGAATTTCTTTCAGCTCTTGGTCTGGTCTCTTCTCACTTCTGTTCAGGTG	420
FILING DATE: 16-JUNE-1992	Db	361	CATACCTGGAATTTCTTTCAGCTCTTGGTCTGGTCTCTTCTCACTTCTGTTCAGGTG	420
APPLICATION NUMBER: US 07/275,433	Qy	421	TTATCCACGTGACCAAGGAAGTAAAGAAAGTGGCAACCGCTGTCCTGTGTCAATGTTT	480
FILING DATE: 23-NOV-1988	Db	421	TTATCCACGTGACCAAGGAAGTAAAGAAAGTGGCAACCGCTGTCCTGTGTCAATGTTT	480
ATTORNEY/AGENT INFORMATION:	Qy	481	CTGTTGAAGAGCTGGCAACAACTCGATCTACTGCGAAAGGAGGAGGAAAATGGTCTGA	540
NAME: Mandragouras, Amy E.	Db	481	CTGTTGAAGAGCTGGCAACAACTCGATCTACTGCGAAAGGAGGAGGAAAATGGTCTGA	540
REGISTRATION NUMBER: 36,207	Qy	541	CTATGATGTCTGGGACATGAATATATATGCGCCGAGTACAAGAACCGACCATCTTTGATA	600
REFERENCE/DOCKET NUMBER: RPI-002CP4	Db	541	CTATGATGTCTGGGACATGAATATATATGCGCCGAGTACAAGAACCGACCATCTTTGATA	600
TELEPHONE: (617) 227-7400	Qy	601	TCATAATTAACCTCTCCATTTGATCCTGGCTCTGGCCCATCTGACGAGGGGACATACG	660
TELEFAX: (617) 227-5941	Db	601	TCATAATTAACCTCTCCATTTGATCCTGGCTCTGGCCCATCTGACGAGGGGACATACG	660
INFORMATION FOR SEQ ID NO: 1:	Qy	661	AGTGTGTTGTTCTGAAGTATGAAAAGAGCGCTTTCAAGCGGGAACACCTGGCTGAAGTGA	720
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TOPOLOGY: linear	Db	781	CTAATATTAGAAGGATAATTTGCTCAACCTCTGGAGGTTTTCCAGAGCCCTCACCTCTCT	840
MOLECULE TYPE: cDNA to mRNA	Qy	841	GGTTGAAAATGGAGAAAGTAATTAATGCCATCAACACACAGTTTCCCAAGATCCCTGAAA	900
HYPOTHETICAL: no	Db	841	GGTTGAAAATGGAGAAAGTAATTAATGCCATCAACACACAGTTTCCCAAGATCCCTGAAA	900
ANTI-SENSE: no	Qy	901	CTGAGCTCTATGCTGTAGAGCAAACTGGATTTCAATATGACCAACCAACCAAGTTCA	960
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ORGANISM: Homo sapien	Qy	961	TGTGCTCTCATCAAGTATGGACATTTAAGAGTGAATCAGACCTTCACTGGAATACACCA	1020
TISSUE TYPE: lymphoid	Db	961	TGTGCTCTCATCAAGTATGGACATTTAAGAGTGAATCAGACCTTCACTGGAATACACCA	1020
CELL TYPE: B Cell	Qy	1021	AGCAAGAGCATTTTCTGATTAACCTGCTCCCATCTGGGCCATTTACCTTAATCTCAGTAA	1080
CELL LINE: Raji	Db	1021	AGCAAGAGCATTTTCTGATTAACCTGCTCCCATCTGGGCCATTTACCTTAATCTCAGTAA	1080
IMMEDIATE SOURCE:	Qy	1081	ATGGAATTTTGTGATATGCTGCTGACCTACTGCTTTTCCCAAGATGCAGAGAGAAA	1140
LIBRARY: cDNA in pCDM8 vector	Db	1081	ATGGAATTTTGTGATATGCTGCTGACCTACTGCTTTTCCCAAGATGCAGAGAGAAA	1140
CLONE: B7, Raji clone #13	Qy	1141	GGAGGAATGAGAGATTGAGAAAGGAAAGTGTACGCCCTGTATTAACAGTGTCCGAGAGC	1200
POSITION IN GENOME:	Db			
CHROMOSOME/SEGMENT: 3				
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NAME/KEY: Open reading frame (translated region)				
LOCATION: 318 to 1181 bp				
IDENTIFICATION METHOD: similarity to other pattern				
NAME/KEY: Alternate polyadenylation signal				
LOCATION: 1474 to 1479 bp				
IDENTIFICATION METHOD: similarity to other pattern				
PUBLICATION INFORMATION:				
AUTHORS: FREEMAN, GORDON J.				
AUTHORS: FREEDMAN, ARNOLD S.				
AUTHORS: SEGIL, JEFFREY M.				
AUTHORS: LEE, GRACE				
AUTHORS: WHITMAN, JAMES F.				
AUTHORS: NADLER, LEE M.				
TITLE: B7, A New Member Of The Ig Superfamily With				
TITLE: Unique Expression On Activated And Neoplastic B Cells				
JOURNAL: The Journal of Immunology				
VOLUME: 143				
ISSUE: 8				
PAGES: 2714-2722				
DATE: 15-OCT-1989				
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1491				
US-08-592-711-1				
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Best Local Similarity 100.0%; Pred.No. 0;				
Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db 1 CCAAGAAAAGTGTGTTGCTTATAGACTGTAAAGAGAACATCTCAGAGT 60				

GenCore version 5.1.6
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Run on: March 20, 2004, 15:17:35 ; Search time 555.527 Seconds

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Perfect score: 1491

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1491	100.0	1491	9	US-09-837-867A-18	Sequence 18, Appli
3	1491	100.0	1491	10	US-09-962-969-18	Sequence 18, Appli
4	1491	100.0	1491	10	US-09-350-202-1	Sequence 1, Appli
5	1491	100.0	1491	10	US-10-261-101-1	GENERAL INFORMA
6	1491	100.0	1491	14	US-10-126-088-1	Sequence 1, Appli
7	1491	100.0	1491	15	US-10-390-330-1	Sequence 1, Appli
8	1489.4	99.9	1549	9	US-09-772-102-13	Sequence 13, Appli
9	895.4	60.1	8578	9	US-09-828-825-1	Sequence 13, Appli
10	895.4	60.1	8578	9	US-09-828-825-3	Sequence 3, Appli
11	895.4	60.1	8608	9	US-09-828-825-7	Sequence 7, Appli
12	895.4	60.1	8623	9	US-09-828-825-5	Sequence 5, Appli
13	895.4	60.1	8638	9	US-09-828-825-9	Sequence 9, Appli
14	895.2	60.0	8629	9	US-09-828-825-15	Sequence 15, Appli
15	895.2	60.0	8644	9	US-09-828-825-13	Sequence 13, Appli

16	895.2	60.0	8659	9	US-09-828-825-11	Sequence 11, Appli
17	868.2	58.2	879	14	US-10-105-200A-31	Sequence 31, Appli
18	868.2	58.2	879	14	US-10-105-504A-31	Sequence 31, Appli
19	868.2	58.2	879	14	US-10-105-678A-31	Sequence 31, Appli
20	868.2	58.2	879	14	US-10-266-463A-31	Sequence 31, Appli
21	865.4	58.0	867	14	US-10-267-384-207	Sequence 207, Appli
22	865.4	58.0	867	15	US-10-223-507-59	Sequence 59, Appli
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24	851	57.1	867	14	US-10-032-214-47	Sequence 47, Appli
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27	841.4	56.4	867	14	US-10-032-214-159	Sequence 159, Appli
28	841.4	56.4	867	14	US-10-032-214-169	Sequence 169, Appli
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31	835	56.0	868	14	US-10-032-214-35	Sequence 35, Appli
32	835	56.0	868	14	US-10-032-214-40	Sequence 40, Appli
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37	833.4	55.9	868	14	US-10-032-214-45	Sequence 45, Appli
38	832.8	55.9	868	14	US-10-032-214-30	Sequence 30, Appli
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43	831.8	55.8	867	14	US-10-032-214-39	Sequence 39, Appli
44	831.8	55.8	867	14	US-10-032-214-44	Sequence 44, Appli
45	831.8	55.8	867	14	US-10-032-214-150	Sequence 150, Appli

ALIGNMENTS

RESULT 1
US-08-592-711-1
; Sequence 1, Application US/08592711
; Publication No. US20020115214A1
; GENERAL INFORMATION:

APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Renner, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994

CC Raji, clone no. 13. Its position in the genome is chromosome/segment 3.
CC It was published by Freeman, F.J. et al., J. of Immunology, 143: 8: 2714-
CC 2722, 15th October 1989. It can be found in Genbank at Accession no.
CC M27533. The encoded protein, R67989, binds both human CTLA4 and human
CC CD28. It is related to human hb7-2 (see Q81351) and murine hb7 (see
CC Q81372). (Updated on 25-MAR-2003 to correct PN field.)
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XX
DT 13-APR-1999 (first entry)
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DE Human B7 cDNA sequence.
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KW T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis; ds.
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FT sig_peptide
FT /tag= b
FT 420..1181
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XX US5858776-A.
XX
XX 12-JAN-1999.
XX
XX 03-NOV-1993; 93US-00147772.
XX
XX 03-NOV-1993; 93US-00147772.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 11:44:16 ; Search time 629.863 Seconds
(without alignments)
10056.251 Million cell updates/sec

Title: US-09-962-969B-18

Perfect score: 1491

Sequence: 1 CCAAGAGAAAGATGATTCTT.....CTATTAAACACTAATTGAG 1491

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 29Jan04:*

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5: Geneseqn2001bs:*

6: Geneseqn2002s:*

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8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1491	100.0	1491	3	AAAC4051	AAAC4051 Human B 1
6	1491	100.0	1491	4	AAAG9224	AAAG9224 Human B 1
7	1491	100.0	1491	6	ABV72339	ABV72339 Nucleotide
8	1491	100.0	1491	6	ABV52443	ABV52443 Human cDN
9	1491	100.0	1491	6	ABR91632	ABR91632 Human B-1
10	1491	100.0	1491	6	ABD27957	ABD27957 Human B7-
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21	895.4	60.1	8638	6	AAAD31549	AAAD31549 PIREs-hb7
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23	895.2	60.0	8644	6	AAAD31551	AAAD31551 PIREs-II1

24	895.2	60.0	8659	6	AAAD31550	AAAD31550 PIREs-II1
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31	859	57.6	7958	6	AAI72490	AAI72490 H6-promot
32	851	57.1	867	6	ABV94533	ABV94533 Novel co-
33	844.6	56.6	867	6	ABV94508	ABV94508 Novel co-
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ALIGNMENTS

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XX AC AAQ81371;
DT 25-MAR-2003 (revised)
DT 21-AUG-1995 (first entry)
XX DE Human B lymphocyte antigen B7-1 (hB7-1).
XX KW B lymphocyte antigen; B7-1; ss.
XX OS Homo sapiens.
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FT /*tag= b
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XX PD 02-FEB-1995.
XX PF 26-JUL-1994; 94WO-US008423.
XX PR 26-JUL-1993; 93US-00101624.
XX PR 19-AUG-1993; 93US-00109393.
XX PR '03-NOV-1993; 93US-00147773.
XX PA (DAND) DANA FARRER CANCER INST INC.
XX PA (REFK) REFLIGEN CORP.
XX PI Freeman GU, Nadler LM, Gray GS, Greenfield E;
XX WPI; 1995-075236/10.
XX DR P-PSDB; AAR67989.
XX PT Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful for
XX PT enhancing or suppressing T-cell mediated immune responses.
XX PS Disclosure; Page 111-113; 175pp; English.
XX CC Q81371 is in pCDM5 vector. It is derived from lymphoid B cells, cell line


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  Location/Qualifiers
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      source anonymous pool of 6 male brains, age range 23-27; 1
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      oligo-dT primed and directionally cloned (EcoRV site is
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      021. Note: this is a NIH_MGC Library."
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RESULT 2
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2004, 11:47:41 ; Search time 4268.57 Seconds
(without alignments)
10430.790 Million cell updates/sec

Title: US-09-962-969B-18
Perfect score: 1491
Sequence: 1 CCAAGAAAAGTATTGT.....CTATTAACTAATTGAG 1491

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
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 - 5: em_estov:*
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 - 7: em_estro:*
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 - 9: gb_est1:*
 - 10: gb_est2:*
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 - 17: em_gss_hum:*
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 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rpd:*
 - 26: em_gss_pug:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	563.4	37.8	566	9	AV717312 AV717312
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ALIGNMENTS

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DEFINITION 713 bp mRNA linear EST 04-OCT-2001
ACCESSION BI822963
VERSION BI822963.1 GI:15934513
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 713)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://imgc.llnl.gov>
Plate: LLAM11452 row: g column: 08
High quality sequence stop: 711.

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Search completed: March 20, 2004, 18:14:16
Job time : 6059.8 secs

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RESULT 15
A37283
LOCUS A37283 1491 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 23 from Patent WO9404196.
ACCESSION A37283
VERSION A37283.1 GI:2294380
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1491)
AUTHORS Vile, R.G. and Hart, I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 23 03-MAR-1994;
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ACCESSION	AX047041		
VERSION	AX047041.1	GI:11876459	
KEYWORDS			
SOURCE			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Sturboefer, K., Wolf, S.F. and O'Toole, M.		
JOURNAL	Use of soluble cosimulatory molecules to enhance immune responses		
	Patent: WO 0067788-A 1 16-NOV-2000;		
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Best Local Similarity	0; Mismatches 0; Indels 0; Gaps 0;		
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DEFINITION	Sequence 1 from patent US 6653444.		
ACCESSION	AR432549		
VERSION	AR432549.1 GI:40195020		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1491)		
AUTHORS	Freeman, G.J., Freedman, A.S. and Nadler, L.M.		
TITLE	Polypeptides comprising a B7 extracellular domain		
JOURNAL	Patent: US 6653444-A 1 25-NOV-2003;		
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RESULT 12
AR381493

LOCUS AR381493 1491 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6608180.
ACCESSION AR381493
VERSION AR381493.1 GI:40089554
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1491)
AUTHORS Sharpe,A.H., Borriello,F., Freeman,G.J. and Nadler,L.M.
TITLE B7-specific antibodies
JOURNAL Patent: US 6608180-A 18 AUG-2003;
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RESULT 11
AR374162
LOCUS AR374162
DEFINITION Sequence 28 from patent US 6605279.
ACCESSION AR374162
VERSION AR374162.1 GI:40076753
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1491)
AUTHORS Freeman,G.J., Nadler,L.M. and Gray,G.S.
TITLE Therapeutic compositions for inhibiting the interactions of B7-1 and B7-2 with their natural ligands
JOURNAL Patent: US 6605279-A 28-12-AUG-2003;
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR287727
DEFINITION Sequence 1 from patent US 6534055.
ACCESSION AR287727
VERSION AR287727.1 GI:31674733
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1491)
AUTHORS June,C.H., Thompson,C.B., Nabel,G.J., Gray,G.S. and Rennert,P.D.
TITLE Methods for selectively stimulating proliferation of T cells
JOURNAL Patent: US 6534055-A 1 18-MAR-2003;
FEATURES Location/Qualifiers
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1 (bases 1 to 1491)
Sturmhoefel, K., Wolf, S.F. and O'Toole, M.
Use of soluble costimulatory molecules to enhance immune responses
Patent: JP 2002544170-A 1 24-DEC-2002;
GENETICS INSTITUTE INC
OS Homo sapiens (human)
PN JP 2002544170-A/1
PD 24-DEC-2002
PF 05-MAY-2000 JP 2000616813
PI 06-MAY-1999 US 60/132944
PI KNUST STURMHOEFEL STANLEY F WOLF MARGOT O'TOOLE PC
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PC A61P35/00
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DEFINITION Sequence 1 from patent US 6352694.
ACCESSION AR196803
VERSION AR196803.1 GI:20246652
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1491)
AUTHORS June, C.H., Thompson, C.B., Nabel, G.J., Gray, G.S. and Rennett, P.D.
TITLE Methods for inducing a population of T cells to proliferate using agents which recognize TCR/CD3 and ligands which stimulate an accessory molecule on the surface of the T cells


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LOCUS ARI146411 1491 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 18 from patent US 6218510.
ACCESSION ARI146411
VERSION ARI146411.1 GI:15109600
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1491)
AUTHORS Sharpe, A. H., Borriello, F., Freeman, G. J. and Nadler, L. M.
TITLE B7-1 and B7-2 polypeptides
JOURNAL Patent: US 6218510-A 18 17-APR-2001;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION
Sequence 1 from patent US 6149905.
ACCESSION
AR118509
VERSION
AR118509.1 GI:14100419
KEYWORDS
Unknown.
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 1491)
AUTHORS
Ostrand-Rosenberg,S., Baskar,S., Glincher,L.H., Freeman,G.J. and
Nadler,L.W.
TITLE
Tumor cells with increased immunogenicity and uses therefor
JOURNAL
Patent: US 6149905-A 1 21-NOV-2000;
FEATURES
Location/Qualifiers
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Query Match 100.0%; Score 1491; DB 6; Length 1491;
Best Local Similarity 100.0%; Fred. No. 0;
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RESULT 4
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LOCUS AR112769 1491 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 28 from patent US 6130316.
ACCESSION AR112769
VERSION AR112769.1 GI:14092669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1491)
AUTHORS Freeman,G.J., Nadler,L.M., Gray,G.S. and Greenfield,E.
TITLE Fusion proteins of novel CIL4/CD28 ligands and uses therefore
JOURNAL Patent: US 6130316-A 28 10-Oct-2000;
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AR097323
LOCUS AR097323 1491 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6071716.

KEYWORDS: Unknown.
SOURCE: Unknown.

Unclassified.

AUTHORS
Freeman, G.J., Freedman, A.S. and Nadler, L.M.

expression on activated and neoplastic B cells

FEATURES

Location/Qualifiers

Source: */organism*

ORIGIN

Query Match	Score 1491;	DB 6;	Length 1491;
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1

THE UNIVERSITY OF CHICAGO

QY

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Db	1021	AGCAAGAGCATTTTCTGATTAACCTCTCCATCTCCCTGGGCGCATTAACCTTAATCTCAGTAA 1080
Qy	1081	ATGGAATTTTGTGATATGCTGCTCACTTACCTTCTTTCCTCCCAAGATGAGAGAGAGAA 1140
Db	1081	ATGGAATTTTGTGATATGCTGCTCACTTACCTTCTTTCCTCCCAAGATGAGAGAGAGAA 1140
Qy	1141	GGAGGATGAGATTTGAGAGGAAAGTGTAGCCCTGTATTAACAGTGTCCGCAAGC 1200
Db	1141	GGAGGATGAGATTTGAGAGGAAAGTGTAGCCCTGTATTAACAGTGTCCGCAAGC 1200
Qy	1201	AAGGGCTGAAAAGATCTGAAGCTAGCCTCCGTCATCTCTTCTGGATACATGGATCGTG 1260
Db	1201	AAGGGCTGAAAAGATCTGAAGCTAGCCTCCGTCATCTCTTCTGGATACATGGATCGTG 1260
Qy	1261	GGATCATGAGGATTTCTCCCTTACAATTTAAGCTGTTTACCACCTACCTCACCTT 1320
Db	1261	GGATCATGAGGATTTCTCCCTTACAATTTAAGCTGTTTACCACCTACCTCACCTT 1320
Qy	1321	CTTAAACACCTCTTTCAGATTAAGCTGAACAGTTTACAAGATGGCTGGCATCCCTCTCCTT 1380
Db	1321	CTTAAACACCTCTTTCAGATTAAGCTGAACAGTTTACAAGATGGCTGGCATCCCTCTCCTT 1380
Qy	1381	TCCTCCCATATGCAATTTGCTTAATGTAACTCTTCTTTTGGCATGTTTCCCATCTGCCA 1440
Db	1381	TCCTCCCATATGCAATTTGCTTAATGTAACTCTTCTTTTGGCATGTTTCCCATCTGCCA 1440
Qy	1441	TCCTGAATGCTGTCAGCAATTCATTTATTAATAACACATTAATTTGAG 1491
Db	1441	TCCTGAATGCTGTCAGCAATTCATTTATTAATAACACATTAATTTGAG 1491

RESULT 2
AR030782
LOCUS AR030782 1491 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5861310.
ACCESSION AR030782
VERSION AR030782.1 GI:5943996
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1491)
AUTHORS Freeman,G.J., Nadler,L.M. and Gray,G.S.
TITLE Tumor cells modified to express B7-2 with increased immunogenicity and uses therefor
JOURNAL Patent: US 5861310-A 5 19-JAN-1999;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: March 20, 2004, 12:21:06 ; Search time 6054.8 Seconds
(without alignments)
10673.268 Million cell updates/sec
Title: US-09-962-969B-18
Perfect score: 1491
Sequence: 1 CCAAGAAAAGTGATTGT.....CTATTAAACATAATTGAG 1491
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 5940544
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
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- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pin.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_higo_hum.*
- 40: em_higo_mus.*
- 41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1491	100.0	1491	6	AR028770	Sequence AR028770
2	1491	100.0	1491	6	AR030782	Sequence AR030782
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4	1491	100.0	1491	6	AR112769	Sequence AR112769
5	1491	100.0	1491	6	AR118509	Sequence AR118509
6	1491	100.0	1491	6	AR146411	Sequence AR146411
7	1491	100.0	1491	6	AR178603	Sequence AR178603
8	1491	100.0	1491	6	BD272168	Use of so BD272168
9	1491	100.0	1491	6	AR196803	Sequence AR196803
10	1491	100.0	1491	6	AR287727	Sequence AR287727
11	1491	100.0	1491	6	AR374162	Sequence AR374162
12	1491	100.0	1491	6	AR381493	Sequence AR381493
13	1491	100.0	1491	6	AR432549	Sequence AR432549
14	1491	100.0	1491	6	AX047041	Sequence AX047041
15	1489.4	99.9	1491	6	AJ7283	Sequence A37283
16	1489.4	99.9	1491	6	AR091392	Sequence AR091392
17	1489.4	99.9	1491	6	AR178979	Sequence AR178979
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19	1489.4	99.9	1491	9	HUMIGB7	M27533 Human Ig re
20	1489.4	99.9	1549	6	AX204865	Sequence AX204865
21	1222.4	82.0	2824	9	BC042665	Sequence BC042665
22	868.2	58.2	879	6	AR147734	Sequence AR147734
23	868.2	58.2	879	6	AR159756	Sequence AR159756
24	868.2	58.2	879	6	AR160448	Sequence AR160448
25	868.2	58.2	879	6	AR202404	Sequence AR202404
26	868.2	58.2	879	6	AR235981	Sequence AR235981
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33	860.6	57.7	867	6	AX440883	Sequence AX440883
34	851	57.1	867	6	AX440657	Sequence AX440657
35	844.6	56.6	867	6	AX440632	Sequence AX440632
36	843	56.5	867	6	AX440633	Sequence AX440633
37	841.4	56.4	867	6	AX440769	Sequence AX440769
38	841.4	56.4	867	6	AX440779	Sequence AX440779
39	836.6	56.1	867	6	AX440768	Sequence AX440768
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ALIGNMENTS

RESULT 1
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LOCUS AR028770 1491 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5858776.
ACCESSION AR028770
VERSION AR028770.1 GI:5940743
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1491)
AUTHORS Ostrand-Rosenberg, S., Baskar, S., Glimcher, L.H., Freeman, G.J. and Nadler, L.M.
TITLE Tumor cells with increased immunogenicity and uses therefor
JOURNAL Patent: US 5858776-A 1 12-JAN-1999;